

A

MUSCLE-N
m MGGQITRNTIHD-----SIGGSFPVPS-----HRCCHKQKHCPPTLSG-----

BRAIN-N
m NGNNFSSVSSLQRGNEPSRASRG---HPQNLKE-----SIGGSFPVPS-----HRCCHKQKHCPPTLSG----- 55
r NGNNFSSVSSLQRGNEPSRASRG---HPQNLKD-----SIGGSFPVPS-----HRCCHKQKHCPPTLSG----- 55
h NGNNFSSVSSLQRGNEPSRASRG---HPQNLKD-----SIGGSFPVPS-----HRCCHKQKHCPPTLSG----- 55
d MGLSDIPANYMQGSHPHLTLPQQQHHCNQHLQHLQMQQLHNAMPTPAQQAQVLAMESNELLMSTKDKLSSKKMHLKKIKKRFGL 90

NLS1
m -----GGLPATPLLFHPHTKGSQILMDLSHKAVKRQASFCNAITFSNRPLVIEQVRLNITKHQCCNSGALRLGFTSKDPSRIHPD 136
r -----GGLPATPLLFHPHTKGSQILMDLSHKAVKRQASFCNAITFSNRPLVIEQVRLNITKHQCCNSGALRLGFTSKDPSRIHPD 136
h -----GGLPATPLLFHPHTKGSQILMDLSHKAVKRQASFCNAITFSNRPLVIEQVRLNITKHQCCNSGALRLGFTSKDPSRIHPD 136
d VRRSPSSCPGPNNLPLLCFH-SVHGDNIRISRDGTLARRFESFCRAITFSARPVRINERICVRFPAEISNNWNGGIRFGFTSNDP-VTLFG 178

NLS2
m -----GGLPATPLLFHPHTKGSQILMDLSHKAVKRQASFCNAITFSNRPLVIEQVRLNITKHQCCNSGALRLGFTSKDPSRIHPD 136
r -----GGLPATPLLFHPHTKGSQILMDLSHKAVKRQASFCNAITFSNRPLVIEQVRLNITKHQCCNSGALRLGFTSKDPSRIHPD 136
h -----GGLPATPLLFHPHTKGSQILMDLSHKAVKRQASFCNAITFSNRPLVIEQVRLNITKHQCCNSGALRLGFTSKDPSRIHPD 136
d VRRSPSSCPGPNNLPLLCFH-SVHGDNIRISRDGTLARRFESFCRAITFSARPVRINERICVRFPAEISNNWNGGIRFGFTSNDP-VTLFG 178

NHR1
m SLPKYACPDIVSOSGFWAKALPEEFANEENIAFWVDKKSRVFYRINESAAMLFSSGVRTVDFLWALVDVYGLTRGVQLLDS----- 218
r SLPKYACPDIVSOSGFWAKALPEEFANEENIAFWVDKKSRVFYRINESAAMLFSSGVRTVDFLWALVDVYGLTRGVQLLDS----- 218
h SLPKYACPDIVSOSGFWAKALPEEFANEENIAFWVDKKSRVFYRINESAAMLFSSGVRTVDFLWALVDVYGLTRGVQLLDS----- 218
d TLPKYACPDITNREGFWAKALPEEFANEENIAFWVDKKSRVFYRINESAAMLFSSGVRTVDFLWALVDVYGLTRGVQLLDS----- 268

LRS1 *
m SLPKYACPDIVSOSGFWAKALPEEFANEENIAFWVDKKSRVFYRINESAAMLFSSGVRTVDFLWALVDVYGLTRGVQLLDS----- 218
r SLPKYACPDIVSOSGFWAKALPEEFANEENIAFWVDKKSRVFYRINESAAMLFSSGVRTVDFLWALVDVYGLTRGVQLLDS----- 218
h SLPKYACPDIVSOSGFWAKALPEEFANEENIAFWVDKKSRVFYRINESAAMLFSSGVRTVDFLWALVDVYGLTRGVQLLDS----- 218
d TLPKYACPDITNREGFWAKALPEEFANEENIAFWVDKKSRVFYRINESAAMLFSSGVRTVDFLWALVDVYGLTRGVQLLDS----- 268

PKB
m ELVLFDCLRERSFTALRRSLRCEADE-----ARLSVSLCDLNVFGADGDDGAPPAG--CPIPONSLSQHSRALP-A 288
r ELVLFDCLRERSFTALRRSLRCEADE-----ARLSVSLCDLNVFGADGDDGAPPAG--CPIPONSLSQHSRALP-A 288
h ELVLFDCLRERSFTALRRSLRCEADE-----ARLSVSLCDLNVFGADGDDGAPPAG--CPIPONSLSQHSRALP-A 288
d PAAIEPMATVBAQQQMPQBAANASSALNSHHPHQSSRSIPGHIAIEHDLERHVMPSLQSLHLAGNGGSVASVEAAIAHDLANGLPPL 358

NHR2
m QLDG-----DLRFHALRAGAHVRILDEQTVARLEHGRDERALVFTSRPVSAETIFIKVTRSGGGRAGALSFGVTCDFGTLRFADLFPS 373
r QLDG-----DLRFHALRAGAHVRILDEQTVARLEHGRDERALVFTSRPVSAETIFIKVTRSGGGRAGALSFGVTCDFGTLRFADLFPS 373
h QLDG-----DLRFHALRAGAHVRILDEQTVARLEHGRDERALVFTSRPVSAETIFIKVTRSGGGRAGALSFGVTCDFGTLRFADLFPS 373
d RYNANGRLIPVPEHNT-KGRNVLSQDRFVASRTESDFCQGYVETARPTRIGELKIVCVLKTQMYVGALALGLSCNPAMLCENDLEND 447

LRS2 *
m PEALVDRKSEFWAWCR-VPGPLHSGDILGLVYNADGELHLHSHNGAAGMQLCVDASQFLWMLFSLHCAITQVRIIGSTIMTERGGE----- 457
r PEALVDRKSEFWAWCR-VPGPLHSGDILGLVYNADGELHLHSHNGAAGMQLCVDASQFLWMLFSLHCAITQVRIIGSTIMTERGGE----- 457
h PEALVDRKSEFWAWCR-VPGPLHSGDILGLVYNADGELHLHSHNGAAGMQLCVDASQFLWMLFSLHCAITQVRIIGSTIMTERGGE----- 457
d SDFLLDRPEYVWVSKDIAAAPQRGDEIAFFVAPNGEVSISKNNGFVAVVMHVDQSLQWAFLDVYCGSTQSLMFRQQLPNMVAVYSQPQV 537

SP1
m ---SLPCSPASTPTSPSALGIRL-SD-----PLLSTCGSGPLGGSAGG-----TADNSPVSLPESPVTPLGQWSD--- 519
r ---SLPCSPASTPTSPSALGIRL-SD-----PLLSTCGSGPLGGSAGG-----TADNSPVSLPESPVTPLGQWSD--- 519
h ---SLPCSPASTPTSPSALGIRL-SD-----PLLSTCGSGPLGGSAGG-----TADNSPVSLPESPVTPLGQWSD--- 519
d NVNAGSSSSACNAASTSRMLPMTESMSLNAGATAKLLHHPQSLSVAQSTSTLASAGGVNGSRMISMPSNGDILQIQPNNGGCTVLVVNLFP 627

SP2
m ---SLPCSPASTPTSPSALGIRL-SD-----PLLSTCGSGPLGGSAGG-----TADNSPVSLPESPVTPLGQWSD--- 519
r ---SLPCSPASTPTSPSALGIRL-SD-----PLLSTCGSGPLGGSAGG-----TADNSPVSLPESPVTPLGQWSD--- 519
h ---SLPCSPASTPTSPSALGIRL-SD-----PLLSTCGSGPLGGSAGG-----TADNSPVSLPESPVTPLGQWSD--- 519
d NVNAGSSSSACNAASTSRMLPMTESMSLNAGATAKLLHHPQSLSVAQSTSTLASAGGVNGSRMISMPSNGDILQIQPNNGGCTVLVVNLFP 627

RZD
m HMCLCYSCGLRLKKALH-ACCPICRRPIKDIKTVRSS 574
r HMCLCYSCGLRLKKALH-ACCPICRRPIKDIKTVRSS 574
h HMCLCYSCGLRLKKALH-ACCPICRRPIKDIKTVRSS 574
d HMCMCYDCAIEQWRGVGGGQCPICRAVIRDVIRVTT- 754

B

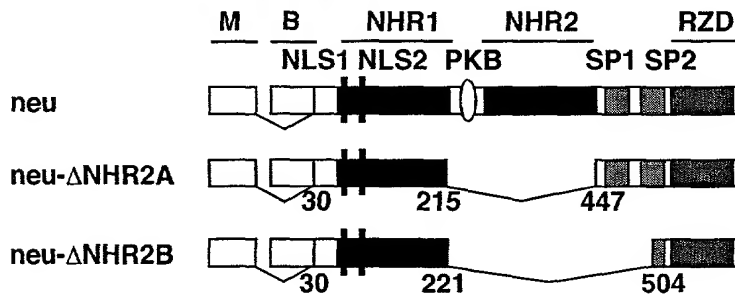
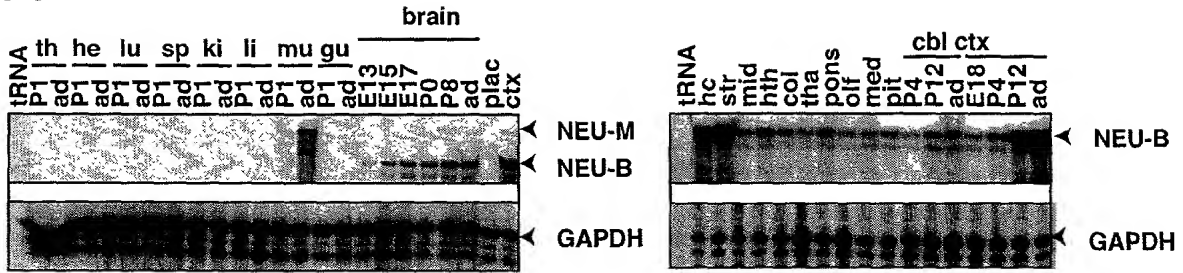


FIGURE 1

A



B

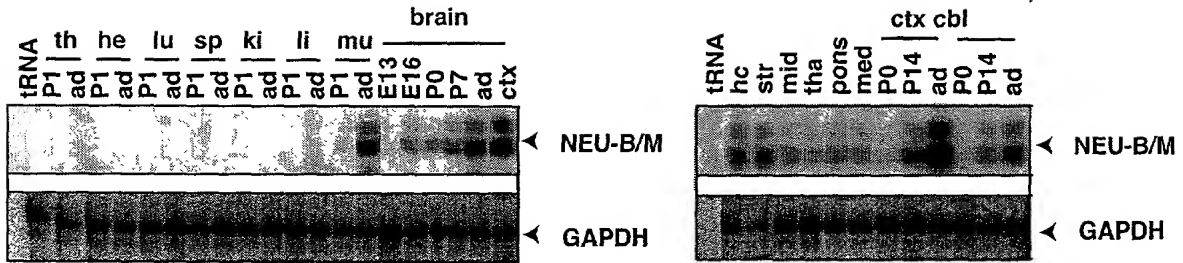


FIGURE 2

Figure 1 consists of three coronal sections of the mouse brain at different developmental stages: E17 (Embryonic Day 17), P7 (Postnatal Day 7), and AD (Adult). The sections show the distribution of 5-HT immunoreactivity, with labels indicating various anatomical structures. In the E17 section, labels include Th (thalamus), PTec (paratenial cortex), SC (superior colliculus), IC (internal capsule), Cb (cerebellum), Me (medulla), P (pons), Pit (pituitary), BG (basal ganglia), and Cx (cortex). In the P7 section, labels include Hc (hippocampus), Cx, BG, and Am (amygdala). In the AD section, labels include Cx, Hc, Th, BG, Am, Pn (pons), and Cb. The immunoreactivity is visible as dark staining in the tissue sections.

FIGURE 3

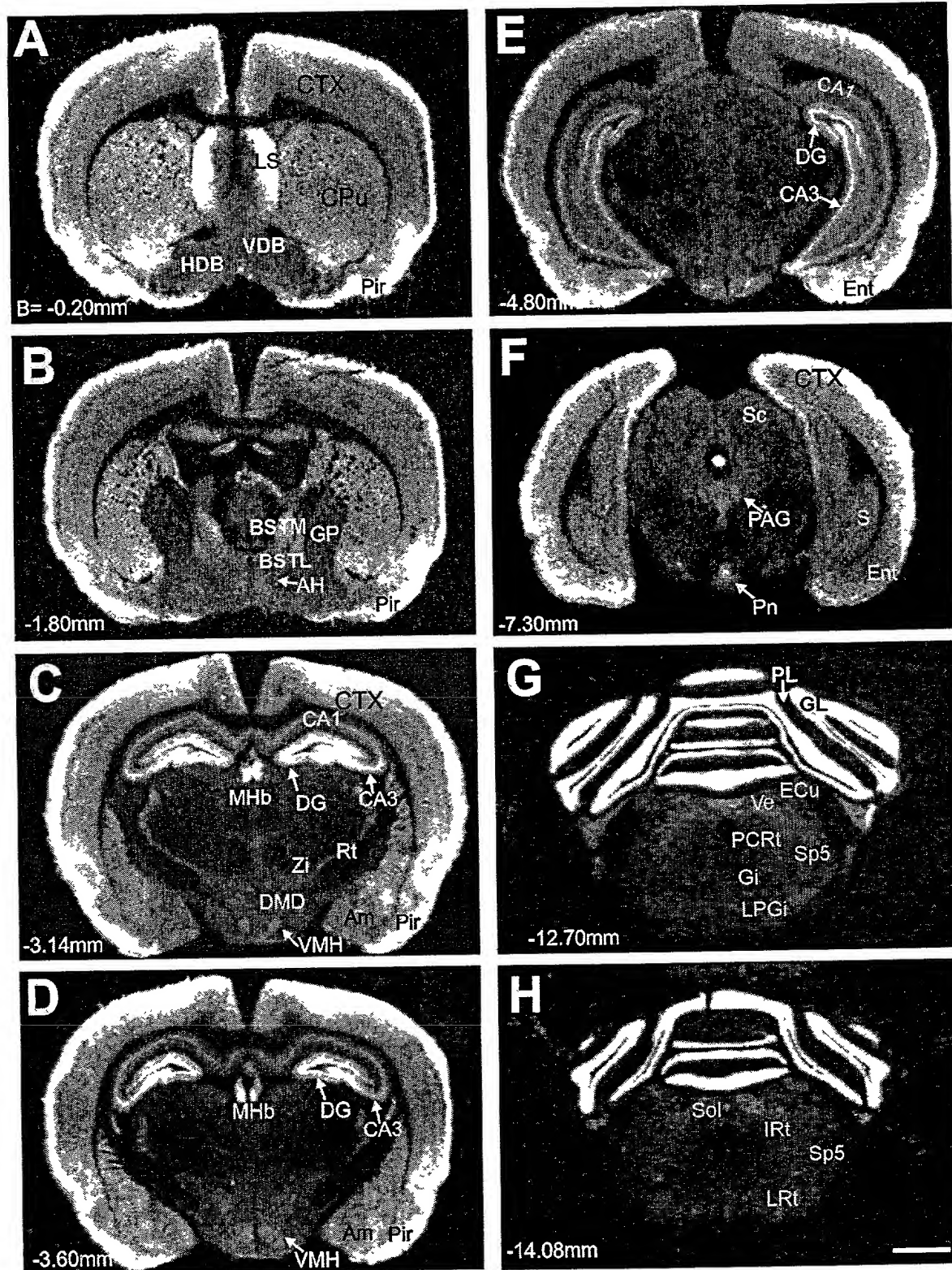


FIGURE 4

Figure 1 consists of 12 panels (A-L) showing autoradiographs of brain sections. The panels are arranged in a 4x3 grid. Each panel is labeled with a letter (A-L) in the top left corner. The panels show the distribution of ³H-thapsigargin in various brain regions, with labels indicating the specific regions: A: CTX; B: Hil, DG, Mol; C: Rad, CA3, Or; D: PoDG, with two arrows pointing to specific cells; E: LS; F: SNc; G: GP; H: Sc; I: Sc; J: DRG; K: GL; L: Pi. A scale bar is present in the bottom right corner of panel L.

FIGURE 6

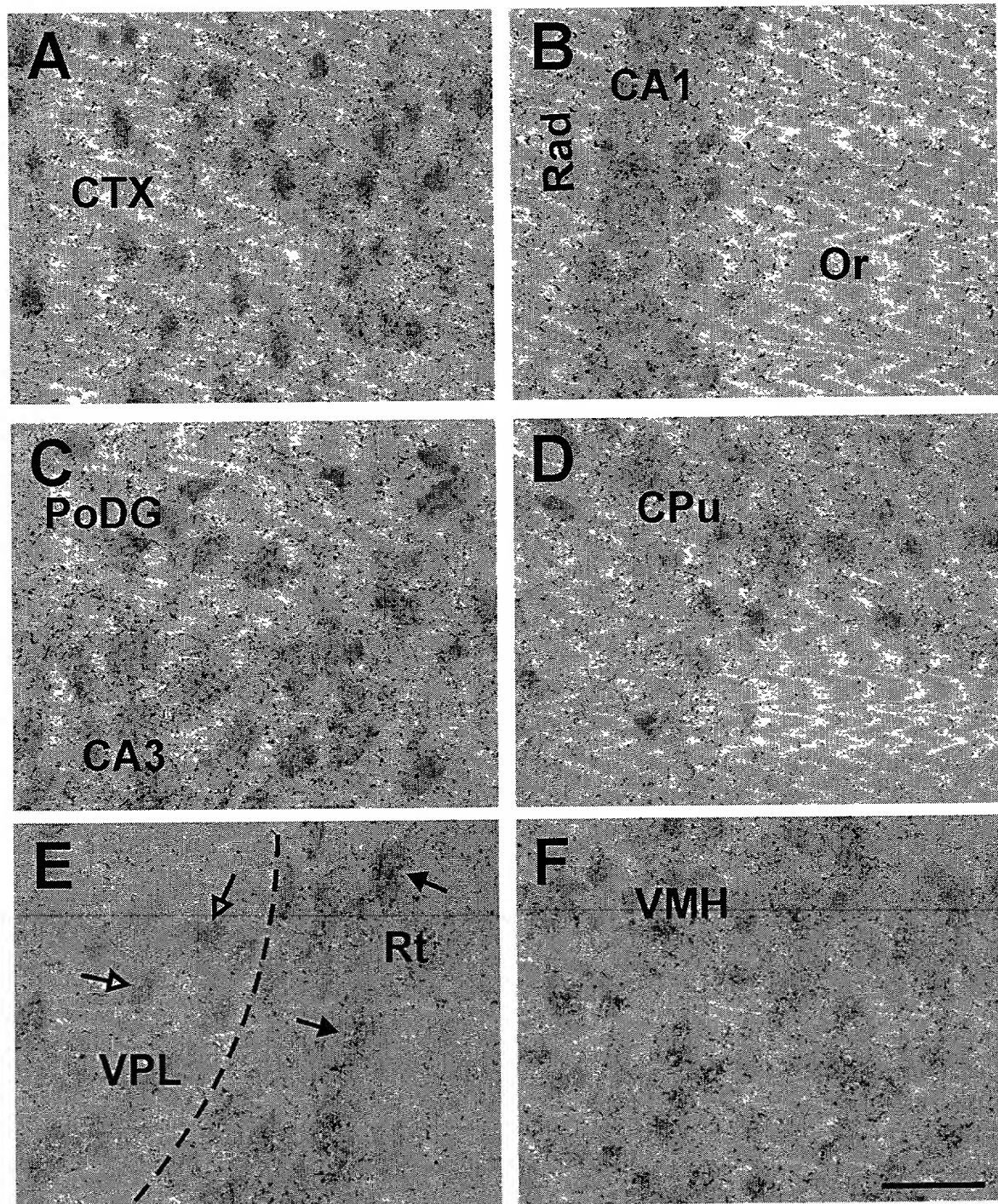


FIGURE 7

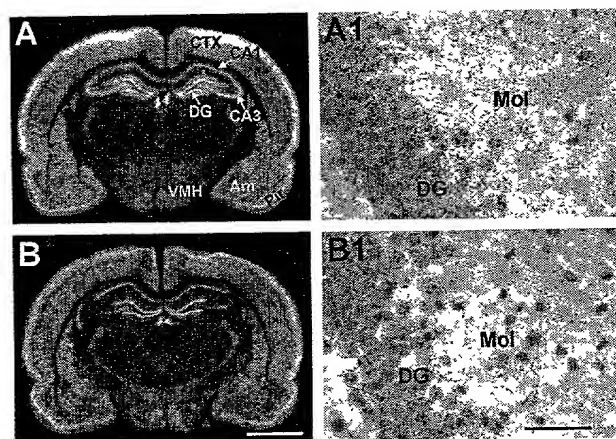


FIGURE 8

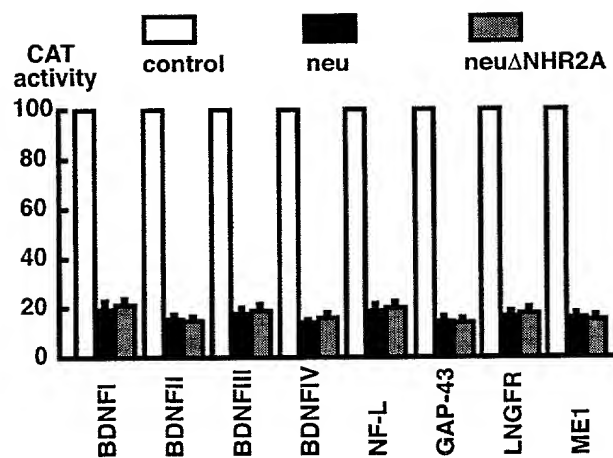


FIGURE 9

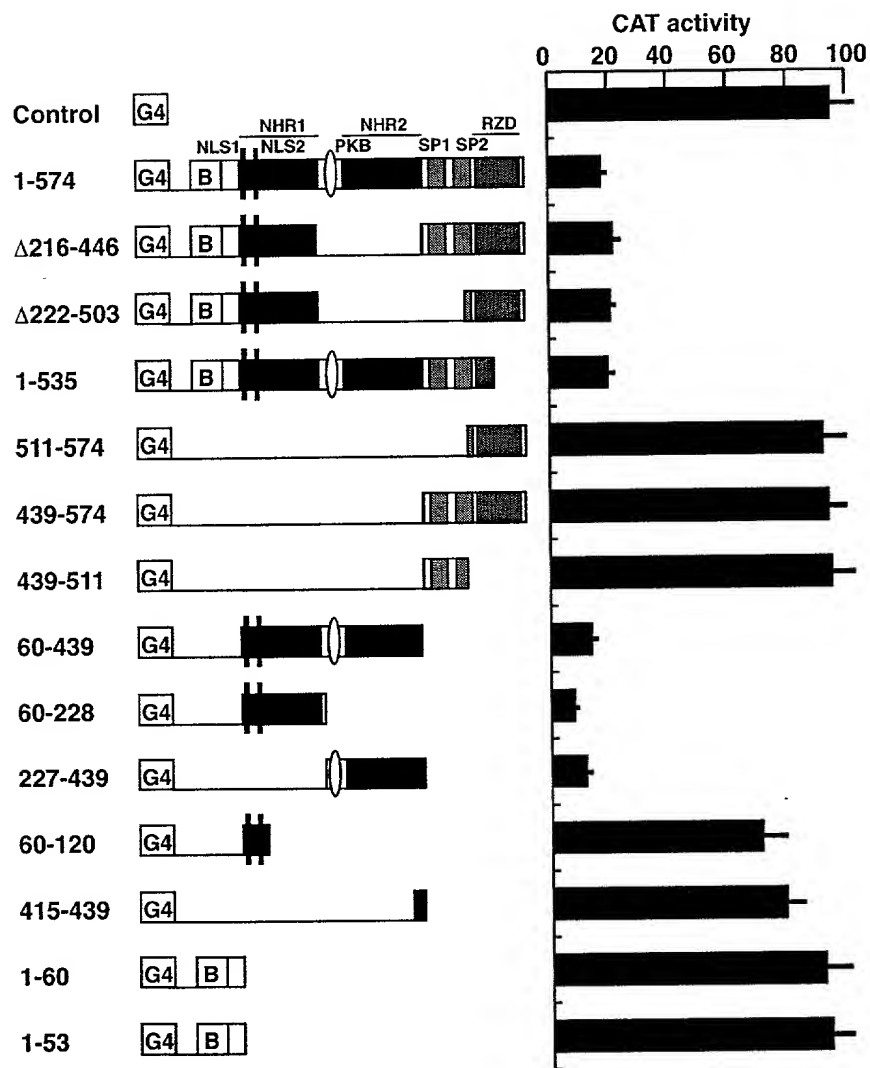


FIGURE 10

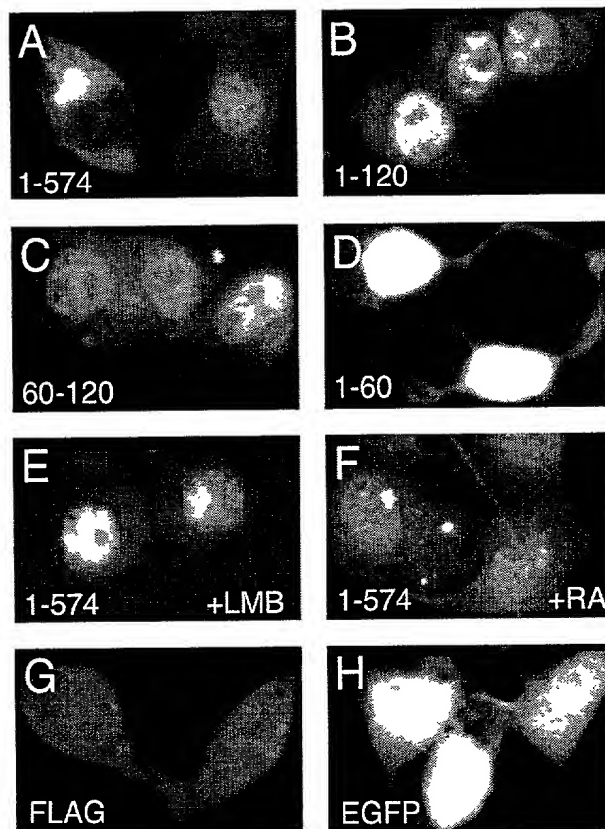


FIGURE 11

h1I FHPHTKGSQILMDLSHKAVKR-QASFCNAITFSNRPVLIYEQVRLKITKKQCCWSGALRL
 h2I FHAQAKGKNVRLDGHSSRRATR-RNSFCNGVTETORPIRLYEQVRLRLVAVRPGWSGALRF
 h3 FHAEAKGAQVRLDTRGCTIAHR-RTTFHDGIVFSORPVRLGERVALRVLREESGWCGGLRV
 dI FHS-VHGDNIRISRDGTIARR-FESFCRAITFSARPVRINERICVKEAEISNNWNGGIRF
 dII FHNTK-GRNVRLSQDRFVASRTESEDFCQGYVETARPIRIGEKLIVQVLKTEQMYVGALAL
 h2II FHATR-GPDVSLSADRKVACAPRPDGGRTLVEFSERPLRPGESLFEVVGPRGLAAPGALAF
 h1II FHALRAGAHVRIILDEQTVARVEHGRDERALVETSRPVRVAETLFVKVTRSGGARPGALSF

h1I GETSKDPSRIHPDSLPHYACPDVLSQSGFWAKAL-PEEFANEENIIAFWVDKKGRVFHRI
 h2I GETAHDPSLMSAQDIPKYACPDVLRPGYAKAL-PENLALRDTVLAYWADRHGRVFYSV
 h3 GETRLDPACVSVPSLPPFLCPDLEEQSPTWAAVL-PEGCALTGDLVRFWVDRREGCLFAKV
 dI GETSNBPVTLEG-TLPKYACPDLTNRPGFWAKAL-HEQYCEKDNILYYYVNGAGDVIYGI
 dII GITSCNPAMLQP-NDLPNDSDFLLDRPEYVWVSKDIAAAPQRGDEIAFFVAPNGEVSISK
 h2II GITSCDPGVLRP-NELPADPDALLDRKEYWVVAR-AGPVPSGGDALSFTLRPGGDVLLGI
 h1II GVTTCBPGTLRP-ADLPFSPEALVDRKEFWAVCR-VPGPLHSGDILGLVFNADGELHLSH

h1I NDSAVMLFFSGVVRTADPLWALVDVYG-LTRGVQLL
 h2I NDGEPVLFHCGVAVGGPLWALIDVYG-ITDEVQLL
 h3 NAGCRLLLREGVPVGAPLWAVMDVYG-TTKAIELL
 dI NNEEKGVILTGTIDTRSLWTVIDIYG-NCTGIEFL
 dII NNGPAVVVMH-VDQSLQLWAFLDVYG-STQSLRMF
 h2II NGRPRGRLLC-VDTTQALWAFFAVRGGVAGQLRLL
 h1II NGAAAGMQLC-VDASQPLWMLLEGLHG-TITQIRIL

FIGURE 12

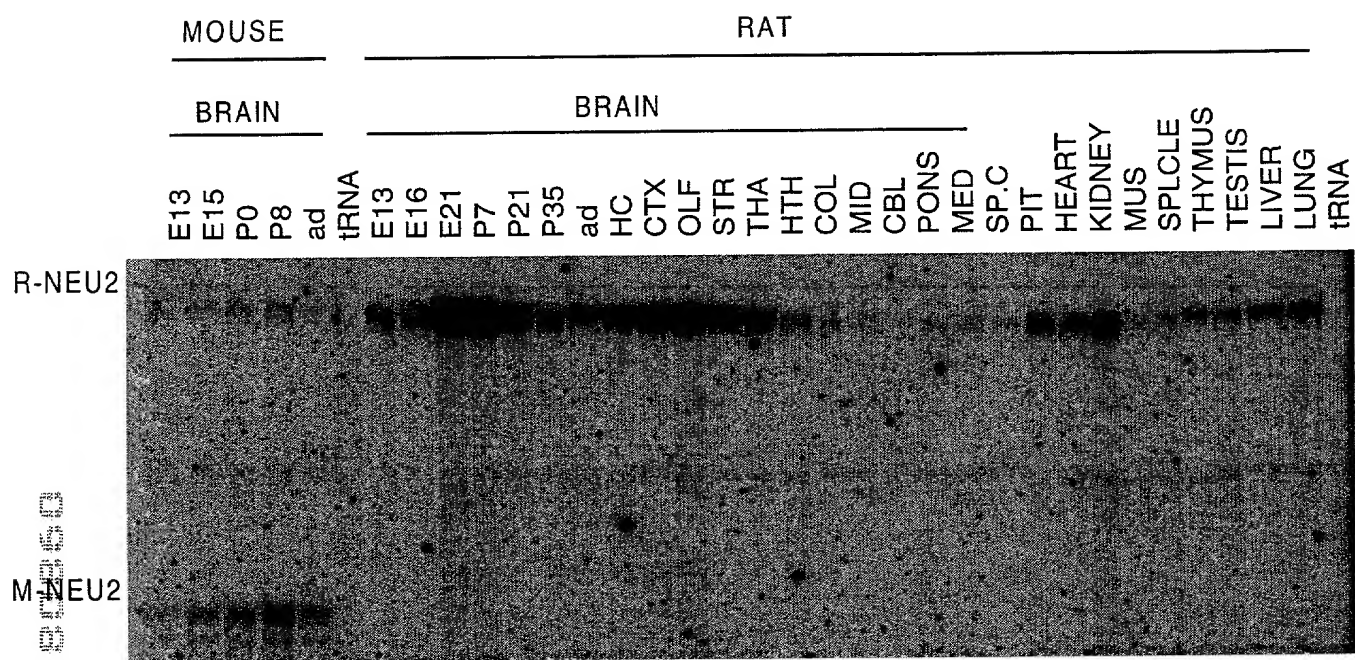


FIGURE 13

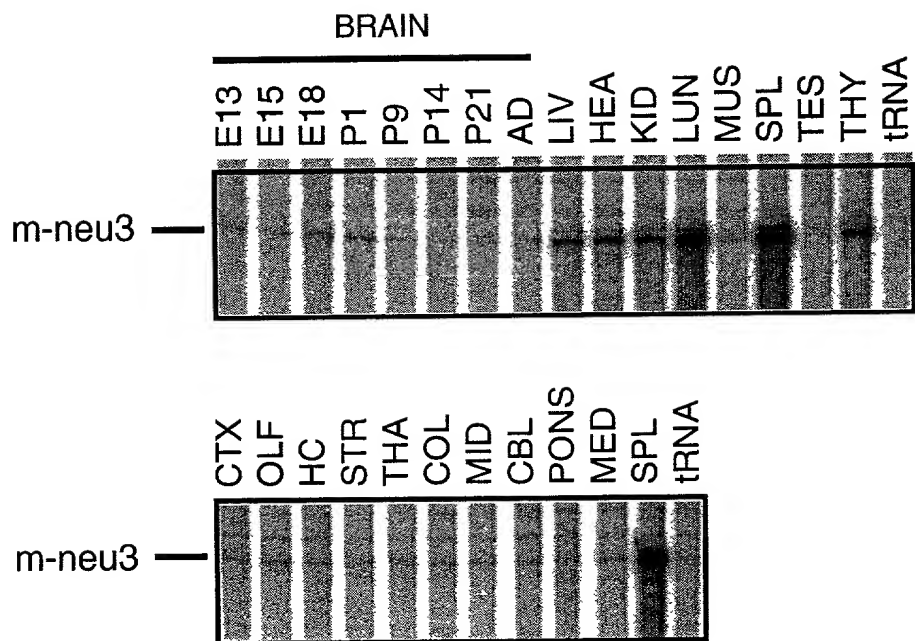


FIGURE 14

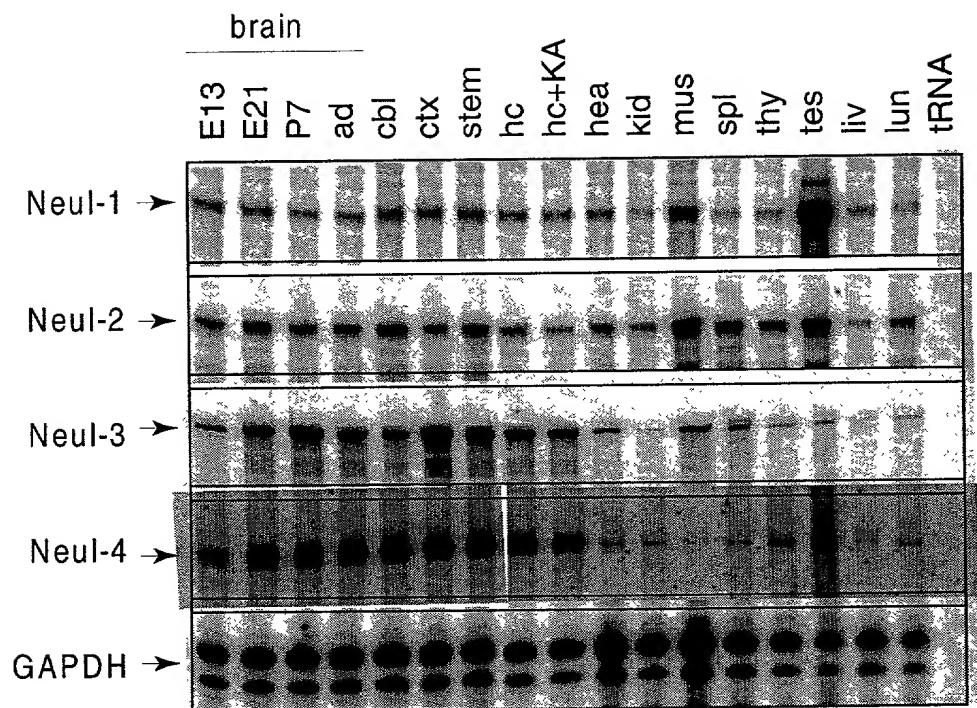


FIGURE 15